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Date: Jun 6, 2001 11:27 PM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

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Search information block:

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Database: Issued_Patents_NA:*  
Database sequences: 302621  
Search time (sec): 76.790000
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; Patent No. 5977337  
; GENERAL INFORMATION:  
; APPLICANT: Loostrom, Sheena M  
; APPLICANT: Du, Run-Pan  
; APPLICANT: Wang, Qun-Jun  
; APPLICANT: Yang, Yan-Ping  
; APPLICANT: Klein, Michel H  
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
; NUMBER OF SEQUENCES: 67  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sim & McBurney  
; STREET: 6th Floor, 330 University Avenue  
; CITY: Toronto  
; STATE: Ontario  
; COUNTRY: Canada  
; ZIP: M5G 1R7  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/867,941  
; FILING DATE: 03-JUN-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Stewart, Michael I  
; REGISTRATION NUMBER: 24,973  
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (416) 595-1155  
; TELEFAX: (416) 595-1163  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2694 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-867-941-2
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Percent Similarity:	41.503	Percent Identity:	18.627

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[illegible]

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1  APPLICANT: Run-Pan Du
2  APPLICANT: Qunjun Wang
3  APPLICANT: Yang, Yan-ping
4  APPLICANT: Klein, Michel H
5  TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
6  NUMBER OF SEQUENCES: 78
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Slim & McBurney
9  STREET: 6th Floor, 330 University Avenue
10 CITY: Toronto
11 STATE: Ontario
12 COUNTRY: Canada
13 ZIP: M5G 1R7
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patentin Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/074,658
21 FILING DATE: 08-MAY-1998
22 CLASSIFICATION: 435
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Stewart, Michael I
25 REGISTRATION NUMBER: 24,973
26 REFERENCE/DOCKET NUMBER: 1038-795
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (416) 595-1155
29 TELEFAX: (416) 595-1163
30 INFORMATION FOR SEQ ID NO: 2:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 2694 base pairs
33 TYPE: nucleic acid
34 STRANDEDNESS: single
35 TOPOLOGY: linear
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37 JS-09-074-658-2

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; Sequence 2, Application US/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loomsore, Sheena M
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; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, Qui-Jun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOPERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330-University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1153
; TELEFAX: (416) 595-1155
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7650 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-867-941-1
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; alignment_scores:
; Quality: 178.00 Length: 918
; Ratio: 0.467 Gaps: 42
; Percent Similarity: 41.503 Percent Identity: 18.627
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; alignment_block:
; US-09-494-297-2 x US-08-867-941-1 ..
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; Align seq 1/1 to: US-08-867-941-1 from: 1 to: 7650
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seq_documentation_block:
; Sequence 1, Application US/09074658
; Patent NO. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: QiuJun Wang
; APPLICANT: Yang, Yan-Bing
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
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; ZIP: M5G 1R7
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; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795

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TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1103
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7650 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-074-658-1

alignment_scores:
      Quality: 178.00      Length: 918
      Ratio: 0.467      Gaps: 42
Percent Similarity: 41.503      Percent Identity: 18.627

alignment block:
US-09-494-297-2 x US-09-074-658-1 ..

Align seg 1/1 to: US-09-074-658-1 from: 1 to: 7650

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seq_documentation_block:

Sequence 69, Application US/09074658

Patent No. 6184371

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M

APPLICANT: Run-Pan Du

APPLICANT: QuiJun Wang

APPLICANT: Yang, Yan-Ping

APPLICANT: Klein, Michel H

TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA

NUMBER OF SEQUENCES: 78

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney

STREET: 6th Floor, 330 University Avenue

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5G 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/074,658

FILING DATE: 08-MAY-1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-795

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 2718 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-074-658-69

alignment_scores:

Quality: 176.00 Length: 796
Ratio: 0.515 Gaps: 40
Percent Similarity: 42.965 Percent Identity: 20.603

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100 ySerArgSerGlyGlnValTyrCysPheAsnLeuLysLysAla..... 114
537 CAGCGAG.....CATGTTTGATGCTTAAACCAATATACAA 574
115 .....PheProLeuGlySerAspSerValLys..... 125
575 TCMAAATATATGTTATGTCGATTCATCACCCTGCCAAAACCCACAC 624
126 .....TyrTyrLysLysHisAspGlyLysSerThrLys.....PheG1 138
625 TACATGATTAATCAACAAGAACAAACATCAAAAAACAAACACGCGCA 674
138 uAspTyrAla.....MetSerProArgLysThr.... 147
675 TGATTTATCAAAAACATTCGTTTGGCTATATGAGCTAAGACGTGACGC 724
148 .....GlyAspGluLeuAsnGlnLysLeuArgAlaValMet 159
725 TAAATAAAAAGTGCACACACACCGACGACACAGAACCGTCCATCTTT 774
160 TyrAsnGly.....HisProGlnAsnAlaAsnGlyLysLeu 171
775 TTCACACACCTACTTATTTATCATGTGAGATGACGACACACCATCT 824
171 tGluGlyLeuGlnProLeuAsnAlaIleArgValThrGlnGluAlaValT 188
825 GCCA.....AAGCGCGTAAATTTGACTATAGAGGCAATT 859
188 rPyrTyrSerAspAsnAlaPro.....IleSerAsnProAsp 200
860 GGTGTATCTGACCGATGTCAAAAAACGCCCATTTTATGATTAACACAG 909
201 Glu.....SerPheLysArgLysSerLys 210
910 GATAAAGTAGGACCTTATTTAACTCAACACGAAATCAATGAAGCGCA 959
210 nLeuValSerThrSerGlnLeuSerLeu..... 219
960 TTTGGTGAAGTCACGACACATTTATCTTAACAGCTTTAAATATTAACCA 1009
220 .....MetArgGlnAla 223
1010 CCCCAGCCATTATAGCGTGACCTTGTCAAAATACCTTAAAGGCCAAA 1059
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1060 TTGCTTATTTATGACAAACCAACAAAGCAAGCGGATGGCGCTTAAAT 1109
240 lProAspAspPhe.....GlnLeuSerLysLeu 250
1110 CAGAAGTCACTTGTATACCGACAAAGGTCATGAATGACCACTGCTATG 1159
250 lSerGluAspLys.....GlyAspLysTyrAsnLysGlyTyrGlnAsn 264
1160 AGATTGACGCCAAGATTATATGCAACCGCTTACTGCGACAGCCAAATCT 1209
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307	LeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheG1	323
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323	naLaarGValPheSerSerAsnAspLe.....G	333
1342	..CGGGTAATTTTATTCCAAGAACCAACCACTTTGTGGCTTTGGTG	1390
333	LYGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsn	349
1391	GCACACGAGACAAACACGACCGAAGCTGTGCCACCAAAAACGGTGATT	1440
350	serPheGlnGlyTyrSerIleAlaClnProIleThrPheLysValGluA1	366
1441	AGT...ACAGAGATTGAA.....AAACCAAGCACACACTTGTGGCA	1481
366	acGlyLysValTyrThrIleIleAspGlyLys.....GlnIleG	379
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379	luAsnProAsnLysGluIleValGluProTyrSerValGluIleArgAsn	395
1532	ATRAATCAAAATTGACAGTCGAACCTGTCCTGTCAGTAATTAAGCATATTAT	1581
396	AspPhe.....GluGluPheSerVa	402
1582	GATATAAATTATGACGACGACCAACAAACAATTCACCAAAAAATAACGC	1631
402	IleuthrThrGlnAsnTyrAla.....LysPheTyrT	413
1632	CAGCGCTCAAAAAAACCCCTTATTTTGGTCAGCATGATAAAGTTTATT	1681
413	YR.....AlaLys.....AsnLysAsnGly	419
1682	TTTAATGGTACTATTATGACTTATGACGCCAAAGAAACCAACAGCTTG6T	1731
420	serSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProProAs	436
1732	GTCTCCCAAGATATACGACGACCAATTAAGAGATTATTTGGCTAAATACCCAGA	1781
436	pSerGluAspGlyGlyLysThrMetThrProAspPheThr.....	450
1782	TGCC.....AAAGTAAGCACAGACAAATTAAGTTACCAAAAAATCG	1819
450	450
1820	TTCTTACACACACCAAGATTAAGCCGTATACCCGATTCATGCCAAAAGC	1865
451GlyGluValLysTyrThrHisIleAlaGlyAr	461
1870	TATGACCAATCAGTTTGGTGAAGTATTTGTTATGATTAACAAAGCAA	1919
461	gasPleuPheLysTyrThrValLysProArgAspThrAspProAspThrP	478
1920	CCCAACACACGATTTATTTGTGCAAGGCGGTCAACGCGATGCAAGTACTC	1965
478	heLeuLys.....His	481
1970	ACCTGCGCCAGTGCAGGTAATTCACCTTAATGCTTTGGGACGGCTAC	2019
482	IleLysValIleGluLysGlyTyrArgIleGluLysGlyGlnAlaIleG1	498
2020	CTGACCCACGAAAAAGACCAAGGTTATGACCAAGATGAGGATCCATCAA	2065
498	uTyrSerGlyLeuThrGluThrGlnLeuArgAlaIleThrGlnLeuAlaI	515

[illegible]

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,402
FILING DATE: 16-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 016921-097
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3531 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-714-402-1

alignment_scores:
Quality: 150.00 Length: 962
Ratio: 0.367 Gaps: 51
Percent Similarity: 42.516 Percent Identity: 19.854

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Align seq 1/1 to: US-08-714-402-1 from: 1 to: 3531

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35 uMetile.....PheAlaLeuValThrSerMetValGlyAlaL 48
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579 GTTGCTGAAATCCCTATATATGGGAAATCATCATGAAGCAGGCGCA 628
48 ysthrValPheGlyLeuValGluSerSerThrProAsnAlaIleAsnPro 64
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629 AAGATGTT.....AGTAGTCTTACAGTTGGAATAATCCC 663
65 AspSerSerGluTyrArgTyrP.....TyrGlyTyr 75
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664 AAAATGTCAGTGTCTTAATATGGAACAAACAGAGTTAGTAGTGC 713
75 rGluSerTyrValArgGlyHisProTyrTyr..... 85
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714 AGCGGATTTTACCGCAACCATGCGGCTATTTTAAATGCTTTGAGT 763
86 ..LysGln.....PheArg 89
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764 TGAACCAAGATAAATCTGAACAAATCAACCCAGGTGATACCTTG 813
90 ValAlaHisPheLeuArgValAsnLeuGluGlySerArgSerTyrGlnVa 106
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814 TTACAGCTGATAGCTGTCATCTCAATCTAAAGT..... 846
106 lTyrCysPheAsnLeuLysAlaPhePro.....L 117
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117 euGlySerAspSerSerValLysLysTyrTyrLysHisAspGlyIle 133
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884 CAATATAGTCCGCTTGCGATGGAATAATACATGCTGAGAACATCACTT 933
134 SerThrLysPheGluAspTyrAla..... 141

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984 TGCAGAAATGAGCTTATTCCTAGAGAAATGAAGAGTGTGGAAATACTA 1033
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155 .....LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnG 169
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169 yIleMetGluGlyLeu.....GluProLeuAsnA 179
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179 lAlleArgValIThrGlnGluAlaValIThrPtyrTyrSerAspAlaPro 195
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205 .ArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetA 221
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1278 TCGTCAAAATCAACGCGACTTAGAAACGACGCTAATATCAATGATGCTG 1327
221 rGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaIThrLysMetPro 237
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244 .....PheGlnLeuSerIlePheGluSerGluAspL 254
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254 ySGlyAspLys..TyrAsnLysGlyTyr..... 262
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1722 ACAGAGTGGCTACGCTTGCTTAAGAAATGTCAACGACATGTGCCAT 1771
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1772 TGCCAGAGGCGGCTTTGAGCTGCTTCATCAATATGTAATAGT...CAG 1818
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1869 GACCTGGGACATATGACCTGTATGAACAAAGCCCAAGGTTATC 1918
355 er..... 355
1919 AGCAGGTGACAGAGAAATGGCGACCTTACTGTGATACCAAACT 1968
356 IleAlaGluProIleThrPhe.....LysValG1 365
1969 GCTGAGGAAATGTCCTCTGGGAAGCCACATTCGTCTGTAAGTAGA 2018
365 uAlaGlyValTyrThrIleIleAspGlyLysGln...IleGluAsn 381
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2217 TAACTACGATGCCAAGATCAGAG..... 2241
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2242 ..TTAAGTACTCAGTGAAGAGTAATGTTCAGACGGCTCAAGGTG 2289
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2487 TCAAGTCAAGCTTATATCTGATGAGTGCGCTGTGAAGGTCAACCAAT 2536
574 yrgInserLeuIleGlyThrGlnThrHisProGlu..... 585
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593 etGluAspLysGluValIle.....ProVal 602
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2731 GAAGAAACGCTCCGCTAGATGATGAGTGTTCAGC.....GCTACAC 2774
619 gThrLysAspPheHisPheGluIleGlu.....LeuLysAsn 632
2775 TACTGTGAAAGACTCAGCCCGAGTTGATACCTTATCAGGTTTATCAAGTG 2824
632 snLysGlnGluLeuLeuSerGlnThrValLysThrAspLys...ThrAsn 647
2825 AGCAAGGTCAAGTCGGTATATGACAAATGAGAAAGATGATGATCCAT 2874
648 LeuGluPheLys.....AspGlyLys.....AlaThr 656
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2925 TATGAGTTGCGTATTCATCTGTTAAACTATTAGTACATGATTTACAG 2974
670 .....LeuProGluGlyTyrSerTyrLeu 677
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678 ValLysGluThrAspSerGluGlyTyrLysVal..... 688
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689 ..LysValAsnSerGlnGluValAlaAsnAlaThrValSerLysThrGly 705
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seq_documentation_block:
; Sequence 8: Application US/08447031A
; Patent No. 5851794
; GENERAL INFORMATION:
; APPLICANT: GUS, Bengt
; APPLICANT: HOOK, Magnus
; APPLICANT: JONSSON, Hans
; APPLICANT: LINDBERG, Martin
; APPLICANT: PARTI, Joseph
; APPLICANT: SIGNAS, Christer
; APPLICANT: SWITLISKI, Lech
; TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL AS
; TITLE OF INVENTION: ITS PREPARATION
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:

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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,031A
FILING DATE: 22-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/861,804
FILING DATE: 21-AUG-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/SE91/00707
FILING DATE: 22-OCT-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: SE 9003374-7
FILING DATE: 22-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300
REFERENCE/DOCKET NUMBER: 012889-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 4612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 931..4485
US-08-447-031A-8

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Quality: 149.00      Length: 774
Ratio: 0.427         Gaps: 41
Percent Similarity: 45.090   Percent Identity: 19.251

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174 .....LeuGluProLeuAsnAlaIleArgValThrGlnGlu 185
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463 .....Leupe... 464
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496 lAlleGlyTyrSerGlyLeuThrGluThrGlnLeuArgAlaIleThrGln 512
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2990 AAGTAAATATACAGTCGAGCAATTAACAAGGTCAAAAGTTATACAA 3039
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
513 .....LeuAlaIleTyrTyrph 518
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3040 CATGTGATTAACAATGATATGCTAATCTGATGTCAGATAAATATAC 3089
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
518 eThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGly 535
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
3090 GCCAGAAACACATCAATTAGTGTGTAAGAAAGTATGGAC..... 3129
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535 heGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGlu 551
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3130 .....GACAAAGACAAT..... 3141
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552 TyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPheIle 568
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3142 .....CAAGTGTAGAGACCAAGAAAGTCACTGAT...TTAT 3182
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568 eProAsnAsnAsnLysTyrGlnSerLeu.....IleGlyThrGln 582
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3183 GCGTGTATGGAGAAAGTAAAGCTTAGACGTCACATCGAAACAACT 3232
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582 rPhISProGluAspLeuValAspIleIleArgMetGluAspLysGlu 598
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3233 GGAAGTACGAA...TTTAAAGACTTACCGAAGTATGAAAGAAAGAA 3279
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599 ValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLe 615
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3280 ATA.....GAATATACAGTGACC..... 3297
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615 uAlaGlyAspArgThrLysAspPheHisPheGluIle..... 627
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3298 .....GAAGTACAGCTAAAGACTACACACAGACATCAAGGTACGACA 3343
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627 ..... 627
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3344 TAACGAACAAGTATACACAGAGAGACATCGGCAACGTAACAAAAAT 3393
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628 ...GluLeuLysAsnAsnLysGlnGluLeuLysSerGlnThrValLysTh 643
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3394 TGGGATGACATATATAACCAAGAGGAAAAAGCAACGTAATCAAAAGT 3443
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643 rAspLysThrAsnLeuGluLysLysAspGlyLys.....A 655
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3444 TGAGTTA.....TATCAAGACGGAAGAAAGCAACAGAAAAAGG 3481
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655 lAthrIleAsnLeuLysHisGlyLysSerLeuThrLeuGlnGlyLeu... 670
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3482 CACACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3531
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671 .....ProGluGlyTyrSerTyrLeuValLysGlu...ThrAs 682
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3532 GAAAAAGCAAAACCAACCAACTAATAATACACAGCTCCAGGAATTAACAA 3581

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682 pSerGluGlyTyrLysValLysValAsnSerGlnGluValAlaAsnAla 699
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3582 GGTCAAGGTTATATACAAACATGTGGATTAACATGATATGGGCACTTGA 3631
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699 hrValSerLys.....ThrGlyThrSerAspGlu 709
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3632 TTGTGACGAATTAATATACGCCAGAAACACATCAATGCGGTGAAAAA 3681
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710 ThrLeuAlaPheGluAsnAsnLysGluProValValProThrGlyValAs 726
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3682 GTATGGAGACACAAAGACATCAAGATGTTAGACAGACCAAGAAAGTCA 3731
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726 pGluLysIle.....AsnGly 731
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3732 TGTAAATTTATGCTAACGCA 3753

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seq_name: /cgnl_7/ptodata/1/lna/5B_COMB.seq:US-08-447-031A-1

seq_documentation_block:

Sequence 1, Application US/08447031A
Patent No. 5851794

GENERAL INFORMATION:

APPLICANT: GUSS, Bengt
APPLICANT: HOOK, Magnus
APPLICANT: JONSSON, Hans
APPLICANT: LINDBERG, Martin
APPLICANT: PATTI, Joseph
APPLICANT: SIGMAS, Christer
APPLICANT: SWITALSKI, Lech
TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL AS
NUMBER OF SEQUENCES: 8
TITLE OF INVENTION: ITS PREPARATION
CORRESPONDENCE ADDRESS:
ADDRESSER: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22113-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,031A
FILING DATE: 22-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/861,804

FILING DATE: 21-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/SE91/00707

FILING DATE: 22-OCT-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SE 9003374-7

FILING DATE: 22-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: McGowan, Malcolm K.

REGISTRATION NUMBER: 39,300

REFERENCE/DOCKET NUMBER: 012889-006

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3827 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-447-031A-1

alignment_scores:

Quality: 148.00 Length: 843
 Ratio: 0.393 Gaps: 43
 Percent Similarity: 44.721 Percent Identity: 19.336

alignment_block:

US-09-494-297-2 x US-08-447-031A-1 ..

Align seg 1/1 to: US-08-447-031A-1 from: 1 to: 3827

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64  ProAspSerSerSerGluTyrArgTyrPtyr.....GlyTyrGlu 76
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694  CCAGAGATGACGACACATGACCATGCTTTTAAATATTAACAATGAAA 743
76  uSerTyrValArgGlyHisProTyrTyrLys.....G 87
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744  AAGTTATGTATCGAAGATATTAATAAGATCAATCAAGGTGAC 793
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87  LnPheArgValAlaHisAspLeuArgValAsnLeuGluGlySerArgSer 103
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794  AGCAGTTAGATTAAAGCATTTAAACATTAATGTGACAGGTACACATAGC 843
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104  Tyr.....GlnValTyrCysPheAsnLeuLysLysAlaPhePr 116
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844  AATTATATATGTGACAAAGTGCATTAATTAATTTGAAAAAGCTTTC 893
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116  oLeuGlySer.....AspSer 122
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894  A...GGTTCAAAATAACTGTGTATATACGAAGAACACAAATGATGTA 940
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122  erValLysLysTyrPtyrLysHisAspGlyLysSerThrLysPheGlu 138
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
941  CAATTCACACAGGCTATGCTATATATATATGTTTCAATTAATCAACAA 990
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139  AspTyrAlaMetSerProArgLysThrGly..... 148
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991  .....ACCAAAATTAACGAATGAACACGAAAAAGCTTGT 1025
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149  .....AspGluLeuAsnG 153
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1026  TAATTAATTCACAGCTGTGTATCAAGACATGTAAGAGAAAGTGAACG 1075
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153  LnlYsLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGly 169
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1076  GGA...TCATTAATCAATACATGTCACAAATATTAATGCAATGCC 1119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
170  LLeuMetGluGly.....LeuGluProLeuAsnAlaIleAr 181
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1120  GGTATTTGAAGTACTGTAAGAAAGTGAATTAAGTTTAAAAACGAGTAA 1169
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181  gValThrGlnGluAlaValTyrTyrSerAspAsnAlaProIleSerA 198
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1170  AGATACCAAG.....GCTCCATTAAC 1192
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198  snProAspGluSerPheLys...ArgGluSerGluSerAsnLeuValSer 213
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1193  AT.....GTAATAATTAACTTCTTAATAAAAGATGATCAGTTGTAAG 1236
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214  ThrSerGlnLeuSerLeuMetArgGlnAlaLeuLysGlnLeuIleAspPr 230
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1237  GACATATCA.....AAGAAATTAAGATTAATTAACAGATGC 1271
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230  oAsnLeuAlaThrLysMetProLysGlnValProAspAspPheGlnLeuS 247
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1272  AAACGGTATTGCTAATATTAAGGTTGCTAGTGAAGACTATATTTTAA 1321
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247  erLlePheGluSerGlu.....AspLysGlyAspLysTyr 258
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1322  AAGAAATTAAGAGCCGACGACCGTATACATTTGTAAGATTAAGAAATAT 1371
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259  .....AsnLysGlyTyrGlnAsnLeuLeuSe 267
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1372  CCGTTTACTATGAAGATACAGATATATCAGGATATTTACGACTATTTGA 1421
267  rGlyGlyLeu.....ValProThrLysProProT 277
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1422  AAATGCAAAAGCGATAGAAAAACAAAAGATGTTCTGCTCAAAAGTTT 1471
277  hrProGlyAspProPheMetProProAsnGlnProGlnThrThrSerVal 293
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1472  GGGAGGCACTCAAAAAGTGAAACCA.....ACGATG 1503
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
294  LeuIleArgLysTyrAlaIleGlyAspTyrSer..... 304
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1504  TATTTCAAGTTGTACAAACAAAGATGACATCAAAATACACACCACTAGA 1553
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305  .....LysLeuLeuGluGlyAlaThrLeuGlnLeuThrGlyA 317
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1554  CAAAGCAGAGATTAAAAATTAAGATGACACGACAAAGTGCATAGT 1603
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317  spAsnValAsnSerPheGlnAlaArgValPheSerSerAsnAsp...Ile 332
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1604  CTATCTT.....CCGAAAAATGACAAAAAT 1629
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333  GlyGluArgLysLeuLeuSerAspGlyThrTyrThrLeuThrGluLeuAs 349
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1630  GGCACGCTATTAA.....TATTTAGTTAAGAAAGTAAA 1664
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349  n.....SerProAlaGlyTyrSerLleAlaGlu... 358
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1665  TGCTCAAGTGACATACAAACACGAGAGATATCAAAAAAGAAATG 1714
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359  .....ProIle...ThrPheLysValGlu 365
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1715  GTTTAGTGGTTACTAATACGAAAAACCAATCGAAACATCAATATAGT 1764
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366  AlAGlyLysValTyrThrLleIleAspGlyLysGlnIleGluAsnProAs 382
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1765  GGTAAAAAAGTATGAGACGACAAAGACATCAAGATGTAAGAACCAAGA 1814
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382  nLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluG 399
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1815  AAAA.....GTCAGTGTGAATTTATGCTAACGGGAGAGA 1849
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399  LnPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyr..... 413
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1850  AAGTAATAAGCTTAAAGACGTGACATCGAACAACCTGGAAGTACGAATT 1899
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414  .....AlaLysAsnLysAsnGlySerSerGlnValValTyrCysPh 427
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1900  AAAGACTTACCGAAGTATGATGAAGGA...AAGAAAAATGACAAATTAAC 1946
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427  eAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrM 444
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1947  GACCGAAGATCAGCTAATAAGACTACACACAGACATCAACGGTACGACA 1996
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444  etThrProAspPheThrThrGlyGluValLysTyrThrHisLleAlaGly 460
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1997  TAACGACAAAGTATACACAGGAGACATCGCCACAAAGTAACAAAAAT 2046
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461  ArgAspLeuPheLysTyrThrValLysProArgAspThrAspProAspTh 477
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2047  TGGATACACATTAATACCAAGACGGAAGAACGACCAACTGAATCAAAAG 2096
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
477  rPheLeuLysHisLleLysLysValIleGluLys..... 488
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2097  TGACTTATATCAAGATGAGAAAGCAACAGCAAAAGCAATATTAAATG 2146
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489  .....GlyTyrArgGluLys 493
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494  GlyGlnAlaIleGluTyrSerGlyLeuThrGlnThrGlnLeuArgAlaAl 510
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2197  GGACACACAGTAATAATACACAGTCGAGGAATTAACAAAGCTCAAGGTTA 2246
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510 aethrgln.....LeuAlaIleT 516
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533 HisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLe 549
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2440 ACAAACTGGAGATACGAA...TTTAAAGACTTACCGAAGATATGATGAAG 2486
596 slySGluValIleProValThrHisAsnLeuThrLeuArgLysThrValT 613
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613 hrgIleuAlaGlyAspArgThrLysAspPheHisPheGluIle.... 627
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627 627
2551 ACACACATAACGAACAGTATACACACAGAGACATCGCAACAGTAC 2600
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2601 AAAAAATTTGGATGACATAATAATACCAAGACGAAAAAGCAACACTGAAA 2650
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2651 TCAAGTTGAGTTA.....TATCAAGATGGAAAAAGCAACAGCA 2688
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2689 AAAACGGCAATATTAAATGAATCTAATACTGGACACATACGTGGACAGG 2738
669 yLeuProGlu.....GlyTyrSerTyrLeuValLysGlu. 680
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2739 ATTATGATGAAAAAGCAAAAGACACAAAGTAAATATACACAGTCGAGAAAT 2788
681 ..ThraspSerGluGlyTyrLysValLysValAsnSerGlnGluValAla 696
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2789 TACCAAAAGTCAAGGTTTATACAAACATGTGATATACATATGATATGGC 2838
697 AsnAlaThrValSerLys.....ThrGlyIleThrse 707
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2839 AACCTTGATTTGTGACGAATAATATACCCAGAAAAACAATCAATTAATCTGC 2888
707 rasPGluThrLeuAlaPheGluAsnAsnLysGluProValValProThrG 724
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2889 TGA AAAAGTATGGAGACGACAAAGCAATCAAGATGTAAGAGACCAAGAAA 2938
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2939 AACCTGATGCAATTTATTTGCTAAACGCA 2967
seq_name: /cgn1_7/ptodata/1/lna/5A.COMB.seq:US-08-703-947-1
seq_documentation_block:
; Sequence 1, Application US/08703947

Patent No. 5788962
GENERAL INFORMATION:
APPLICANT: Wise, Kim S.
APPLICANT: McIntosh, Mark A.
TITLE OF INVENTION: DNA Sequences Coding for Mycoplasma
TITLE OF INVENTION: Hypneumoniae Surface Antigens,
TITLE OF INVENTION: Corresponding Proteins and Use in
TITLE OF INVENTION: Vaccines and Diagnostic Procedures
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grace J. Fishel
STREET: 929 Fee Fee Road, Suite 100
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63043
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
COMPUTER: Hewlett-Packard Vectra
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/703,947
FILING DATE: 28-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,957
FILING DATE: January 17, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Fishel, Grace J.
REGISTRATION NUMBER: 25864
REFERENCE/DOCKET NUMBER: UYW 8141
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314) 878-0440
TELEFAX: (314) 275-7693
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2672 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: region of 5.8 kb HindIII fragment from
DESCRIPTION: genomic library
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Mycoplasma hypneumonae
STRAIN: J
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE: unicellular bacterium
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY: Genomic in Charon 4A, GEN12
CLONE: MhpJ25, MhpJ35, pZJ25, pZJ25.1, pZJ25.14,
CLONE: pZJ35.1, pZJ35.12, pZJ35.13, pZJ35.14
POSITION IN GENOME:
CHROMOSOME/SEGMENT: single chromosome
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: sequence encodes entire 627 amino acids of
NAME/KEY: the structural gene for the surface lipoprotein
NAME/KEY: p65 and includes 312 bp upstream and 479
NAME/KEY: bp downstream of coding sequence
LOCATION: coding sequence for p65 spans 1881 bp of
LOCATION: described sequence (begins at nt 313 and

LOCATION: includes all sequence through nt 2193
IDENTIFICATION METHOD: by similarity to pattern of open reading
IDENTIFICATION METHOD: frame; by experiment identifying protein products of
IDENTIFICATION METHOD: sequence with immune serum to p65
OTHER INFORMATION: immunogenic surface lipoprotein of no known
OTHER INFORMATION: function; C-terminus exposed on external
OTHER INFORMATION: surface of cell
PUBLICATION INFORMATION:
AUTHORS: Mary F. Kim, Manijeh B. Heidari, Susan J.
AUTHORS: Stull, Mark A. McIntosh, and Kim S. Wise
TITLE: Identification and Mapping of an
TITLE: Immunogenic Region of Mycoplasma
TITLE: hypopneumoniae p65 Surface lipoprotein
TITLE: Expressed in Escherichia coli from a Cloned
TITLE: Genomic Fragment
JOURNAL: Infection and Immunity
VOLUME: 58
ISSUE: 8
PAGES: 2637-2643
DATE: August 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: From 1 to 2672

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seq_name: /cgnl_7/ptodata/1/lna/5A_COMB.seq:US-08-480-604A-9
seq_documentation_block:
; Sequence 9, Application US/08480604A
; Patent No. 5736139
; GENERAL INFORMATION:
; APPLICANT: KINK, JOHN A.
; APPLICANT: THALLEY, BRUCE S.
; APPLICANT: PADHYE, NISHA V.
; APPLICANT: FIRCA, JOSEPH R.
; APPLICANT: STAFFORD, DOUGLAS C.
; TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,604A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/422,711
; FILING DATE: 14-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/405,496
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/329,154
; FILING DATE: 25-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,907
; FILING DATE: 02-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/985,321
; FILING DATE: 04-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/429,791
; FILING DATE: 31-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: INGOLIA, DIANE E.
; REGISTRATION NUMBER: 40,027
; REFERENCE/DOCKET NUMBER: OPD-01/63
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7101 base pairs
; TYPE: nucleic acid

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seq_documentation_block:
 ; Sequence 9, Application US/08405496A
 ; Patent No. 5919665
 ; GENERAL INFORMATION:
 ; APPLICANT: WILLIAMS, JAMES A.
 ; TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM

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TITLE OF INVENTION: NEUROTOXIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,496A
FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLTA, DIANE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPBD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..7098
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; Sequence 7, Application us/08867941
; Patent No. 5977337
;
GENERAL INFORMATION:
;
APPLICANT: Loosmore, Sheena M
;
APPLICANT: Du, Run-Pan
;
APPLICANT: Wang, Qui-Jun
;
APPLICANT: Yang, Yan-Ping
;
APPLICANT: Klein, Michel H
;
TITLE OF INVENTION: LACROFERLIN RECEPTOR GENES OF MORAXELLA
;
NUMBER OF SEQUENCES: 67
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: Sim & McBurney
;
STREET: 6th Floor, 330 University Avenue
;
CITY: Toronto
;
STATE: Ontario
;
COUNTRY: Canada
;
ZIP: M5G 1R7
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
;
COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
;
SOFTWARE: Patent Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/08/867,941
;
FILING DATE: 03-JUN-1997
;
CLASSIFICATION: 435
;
ATTORNEY/AGENT INFORMATION:
;
NAME: Stewart, Michael I
;
REGISTRATION NUMBER: 24,973
;
REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: (416) 595-1155
;
TELEFAX: (416) 595-1163
;
INFORMATION FOR SEQ. ID NO: 7:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 2682 base pairs
;
TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; us-08-867-941-7

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Percent Similarity: 41.626      Percent Identity: 19.704

alignment_block:
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348	LeuAsnSerProIaGlyTyTyrSerIleAlaGluProIleThrPheLysVa	364
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454LysTyT	455
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456	ThrHisIleAla...GlyArgAspLeuPhe.....	464
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1899	AACACGCACTATTTTGTGTGCAGAGCGGTAGGCAAGATACCAAGCAAACTT	1948
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511 hrcIleuAlaIeTYrTYrPheThr.....AspSer 521
2083 .....TTCACCCCAAGACATGATGACGATGATTG 2112
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2527 .....GGTTCTTAATCAACAATCAAAAGATATGATGTTAAAGGGCAAT 2569
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seq_name: /cgn1_7/ptodata/1/lna/6B_COMB.seq:US-09-074-658-7

seq_documentation_block:
: Sequence 7, Application us/09074658
: Patent No. 6184371
: GENERAL INFORMATION:
: APPLICANT: Loosmore, Sheena M
: APPLICANT: Run-Pan Du

```

APPLICANT: Quijun Wang
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: Slim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,658
FILING DATE: 08-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2682 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-074-658-7

alignment_scores:
Quality: 138.00 Length: 812
Ratio: 0.408 Gaps: 39
Percent Similarity: 41.626 Percent Identity: 19.704

alignment_block:
US-09-494-297-2 x US-09-074-658-7 ..

Align seg 1/1 to: US-09-074-658-7 from: 1 to: 2682

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531 CCATCGT...TTTGACCCCAAGATAAACACCATTAAGTGTATGTT 577
117 EUGLY.....SERASPSERVALYSLYSTYRGLYSLYSHISASP 131
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578 ATGCTAACTTAACACACCATCCACACACACTCACATCAATCAATCAG 627
132 GLYIleSerThyLysPheGluAspTyrAlaMetSerPro..... 144
628 CAGGCTATATATAAGAAAATAACAAAGCCGTGTGACCTTATGAAAATAT 677
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678 CCGTTTGGTATCTTGACTACAAAGACAGAGCCGTGACCCAAAAAATG 727
155 .....LeuArgAlaVal 158
728 CCGATATATCAAAATGACCAAGACCGCATTCACCAAAACCATGCCATTTTG 777
159 MetTyrAsnGlyHisProGlnAsnAlaAsnGlyTleMetGluGlyLeuG1 175
:::|||||::::::|||||:::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::~
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194 AlaProIleSerAsnProAspGluSerPheLysArgGluSerLysSerAs 210
922 AGTGGCAAAAGCCAAC.....GAGGCGGA 944
210 nLeuValSerThSerGlnLeuSerLeuMetArgGlnAlaLeuLysGln 227
945 TGTCGTCAGTGGCCGCCACATTTATCTAAAGCGCTTCAATATATACAC 993
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994 .....ACGCTGCCACTTATCAGGTGAGTATTTTGAC 1023
244 Phe.....GlnLeuSerIlePheGluSerGluAspLysG1 255
1024 ACAAACTCATTAACAGGCAAGCTGCTCTATTATGACAAATCCCATGAG.. 1071
255 YASPLYSTYFASNLYSGLY..... 261
1072 .....CAAAATATATTAAGCGCAATATCTCAAAAGCCAATTGGACACTACA 1117
262 .....Tyrgln..... 263
1118 AAAAGTCATGAAGAACCGATGTATCAATATGATGCCAAATCAACGGT 1167
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1168 ACCGCTTTGTGCGTACGGCCAAATCTTGTGTTATGAGAAACACACAAAC 1217
277 rProGly.....AspProPromeLProProAsnGlnP 288
1218 CGCACCTTTTATCAAGAGCTGTTCTCCAAAAGCAACCCCAATATAC 1267
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1268 CAAACCTTAAT.....TCA 1281
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seq_documentation_block:
; Sequence 6, Application US/08867941
; Patent No. 5977337
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Du, Run-Pan
; APPLICANT: Wang, QuiJun
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; City: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,941
; FILING DATE: 03-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-867-941-6
alignment_scores:
Quality: 138.00 Length: 812
Ratio: 0.408 Gaps: 39
Percent Similarity: 41.626 Percent Identity: 19.704

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Alignment block:

US-09-494-297-2 x US-08-867-941-6 ..

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1319  AACCGCTTTGTGCTAGCGCAAAATCTTGTGTTATATGAGAAAACAACAAC 1368
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277  rProGly...AspProProMetProProAsnGlnP 288
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1478  ....GCGGTAAATTTTATCCATATGACAAAGCATCTTATGTGCTGT 1520
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333  ....GlyLysArgLLeGluLeuSerAspLysThrTyrThrLeuThrGlu 347
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    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
348  LeuAsnSerProAlaGlyTyrSerLLeAlaGluProLLeThrPheLysVal 364
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1571  TATTTTATGT...GCAGGCTTTGAA...AAACCCAGCACCGATTGTTGT 1611
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
364  LgluAlaGlyLysValTyrThrLLeLeuAspGlyLysGlnLLeGluAsnP 381
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1612  GGATTAATGAACGATTGTGTGATTTATGACCGTAAAGGTTAAATATATC 1661
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
381  ro...AsnLysGluLeuValGluProTyrSerValGluAlaTyr... 394
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1662  ACATTAATGAAGATGAATATATCCAGTGTATGATATATATATGATAT 1711
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
395  .....AsnAspPheGluGluPheSerValLeuThrP 405
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1712  ACTTTGGGCGCAAGCAGAGAGAGCAGTTACCCAAAAGTCAGCAGCGCAC 1761
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
405  rGln...AsnTyrAlaLysPheTyrTyrAlaL 415
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1762  CCAAGTCGTGCCAGCTTATTTTGGGCAACATGATTAATTTTATTTT... 1807
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
415  yAsnLysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeu 431
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1808  ....AATGGCACTATATATGACCTATACACCACTGCTGTGTGATATA 1849
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
432  LysSerProProAspSerGluAspGlyGlyLysThrMetThrProAspH 448
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1850  TTAGCCCTCGCTCCGATGCTGTCAAAAGCCAAACCATTAAGAAAAATA 1899
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
448  eThrThrGlyGluVal... 453
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1900  CCTTAATGCCACACTAATAAAGACAAACCAAGTTACCGCCATGCTGTCTAC 1949
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
454  .....LysTyr 455
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
1950  AAGAAGCCAAAGATATAAGCTTATACCGCCATTCGTGCCAAAAGCTAT 1999
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
456  ThrHisLLeAla...GlyArgAspLeuPhe... 464
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2000  CAGCAATCATGATTTTGGCAGACGCTGTATATACAGATCCAAACCAACCC 2049
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
465  ....LysTyrThrValLysProArgAspThrAspProAspThrPheL 479
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2050  AACACGCAAGTTATTTTTCGACAGCGGTAGGCGCAGATACACACACACTT 2099
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
479  euLysHisLLeLysValLe... 486
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2100  TGCCCCAGCGAGTAATATCACTACAAAGGTCTTTGGCAGGCTACCTGT 2149
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
487  .....GluLysGlyTyrArgGluLysGlnAlaLLeGluTyr 499
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2150  ACCCAAAAAGGACAAAGGTTATATAGGATTAATGCAAAACCATCAAGGA 2199
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499  rSerGly...LeuThrGluThrGlnLeuArgAlaLal 511
    |||:::|||||:::|||||:::|||||:::|||||:::|||||:::
2200  AAAAGTATCATCAGGTTATCTGTATACCGAAAAAC... 2233
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511 hrglnleuAlaIleTyrPheThr.....AspSer 521
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2234 .....TTCACCCGAGAGTGAATGACGATGATTG 2263
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522 AlaGlnleuAspLysAspLysleuLysAspTyrHisGlyPheGlyAspMe 538
      ||| ||| ||| ||| ||| ||| ||| |||
2264 ACCGATCTGATGATTCACAAGATGATATACATGCGCATGATGATT 2313
      ||| ||| ||| ||| ||| ||| ||| |||
538 tAsnAspSerThrleuAlaValAlaLysIleLeuValGluTyrAlaGlnA 555
      ||| ||| ||| ||| ||| ||| ||| |||
2314 G.....ATTGCATCTGATGATTCACAAG 2336
      ||| ||| ||| ||| ||| ||| ||| |||
555 sPseAsnProPheGlnleuThrAspLeuAspPhePheIleProAsn 571
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2337 ATGATGACGAGATGAGATGACGATTCAGATGATTG.....GGTCAT 2380
      ||| ||| ||| ||| ||| ||| ||| |||
572 AsnLysTyrGlnSerleuIleGlyThrGlnThrHisProGlnAspLeuA 588
      ||| ||| ||| ||| ||| ||| ||| |||
2381 GGTCGACATGATGACGCGCGCAAGGTATCATGACAGTAT..... 2425
      ||| ||| ||| ||| ||| ||| ||| |||
588 LAspIleIleArgMetGluAspLysGluValIleProVal..... 602
      ||| ||| ||| ||| ||| ||| ||| |||
2426 .....ATTGCGCCCTGATTTGAAACAATACTGCCCATTAATGAGC 2468
      ||| ||| ||| ||| ||| ||| ||| |||
603 ..ThiHisAsnleuThrleu..... 608
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2469 CTACTCATGAAAAAAGCTTGGCCCTAGATGTAATAAAGCTTAAGTTT 2518
      ||| ||| ||| ||| ||| ||| ||| |||
609 .....ArgLysThrValThrGlyLeuAlaGlyAspArgTh 620
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2519 GAATGATTTTAAACACACAGCCTAAGTGTAAATTAACGATGAGAG 2568
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620 rLysAspPheHisPheGluIleGluLeuLysAsnLysGlnleuL 637
      ||| ||| ||| ||| ||| ||| ||| |||
2569 AGGTATATGCTCTTGTATATC.....AAAAATGCCAAATTTGATGCA 2612
      ||| ||| ||| ||| ||| ||| ||| |||
637 euserGlnThrValLysThrAspLysThrAsnleuGluPheLysAspGly 653
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2613 CAGGATTTTACCGCCAAAGCCGATGTGCCAACTATGCGTAAGAAGTGGT 2662
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654 LysAlaThrIleAsnleuLysHisGlyLysSerleuThrleuGlnGlyLe 670
      ||| ||| ||| ||| ||| ||| ||| |||
2663 .....AACAAACCAAGTGC..... 2677
      ||| ||| ||| ||| ||| ||| ||| |||
670 uProGlnGlyTyrSerTyrleuValLysGluThrAspSerGlnGlyTyrL 687
      ||| ||| ||| ||| ||| ||| ||| |||
2678 .....GGTTCTTATCAACAATCAAGATATGATGTTAAGGGCAAT 2720
      ||| ||| ||| ||| ||| ||| ||| |||
687 yValLysValAsnSerGlnGluValA..... 696
      ||| ||| ||| ||| ||| ||| ||| |||
2721 TTTTGGCACAAATGGCGAAGAGTGGCAGACAGTACATCATGACAAA 2770
      ||| ||| ||| ||| ||| ||| ||| |||
697 .....AsnAlaThrValSerLysThrGly 704
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2771 GCGGATGCAATCATGACACCGCGCAAAAAGACAGG 2806

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seq_name: /cgnl_7/prodata/1/lna/bb_COMB.seq:us-09-074-658-6

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seq_documentation_block:
; Sequence 6, Application us/09074658
; Patent No. 6184371
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena M
; APPLICANT: Run-Pan Du
; APPLICANT: Quljun Wang
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Klein, Michel H
; TITLE OF INVENTION: LACTOPERRICIN RECEPTOR GENES OF MORAXELLA
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Slim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto

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; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/074,658
; FILING DATE: 08-MAY-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-795
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7641 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-09-074-658-6
;
; alignment_scores:
; Quality: 138.00 Length: 812
; Ratio: 0.408 Gaps: 39
; Percent Similarity: 41.626 Percent Identity: 19.704
;
; alignment_block:
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; Align seg 1/1 to: US-09-074-658-6 from: 1 to: 7641
;
; 84 TTTTGTGTCGlnPheArgValAlaHisAspLeuArgValAsnleuGlnG 100
; ||| ||| ||| ||| ||| ||| ||| |||
; 632 TATTTTAAACAATCCCGTCATGTCGATGTTGCACCTAGACAGTGAAG 681
; ||| ||| ||| ||| ||| ||| ||| |||
; 100 ySerArgSerTyrGlnValTyrCysPheAsnleuLysAlaPheProL 117
; ||| ||| ||| ||| ||| ||| ||| |||
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; ||| ||| ||| ||| ||| ||| ||| |||
; 117 euGly.....SerAspSerSerValLysLysTyrTyrLysHisAsp 131
; ||| ||| ||| ||| ||| ||| ||| |||
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; ||| ||| ||| ||| ||| ||| ||| |||
; 132 GlyIleSerThrLysPheGluAspTyrAlaMetSerPro..... 144
; ||| ||| ||| ||| ||| ||| ||| |||
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; ||| ||| ||| ||| ||| ||| ||| |||
; 145 .....ArgIleThrGlyAspGluLeuAsnGlnLys... 154
; ||| ||| ||| ||| ||| ||| ||| |||
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; ||| ||| ||| ||| ||| ||| ||| |||
; 155 .....LeuArgAlaVal 158
; ||| ||| ||| ||| ||| ||| ||| |||
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; ||| ||| ||| ||| ||| ||| ||| |||
; 159 MetTyrAsnGlnLysProGlnAsnAlaAsnGlyIleMetGlnGlyLeuG 175
; ||| ||| ||| ||| ||| ||| ||| |||
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; ||| ||| ||| ||| ||| ||| ||| |||
; 175 uProLeuAsn..... 178
; ||| ||| ||| ||| ||| ||| ||| |||
; 973 TAAATTTAACTAACACAGCAAGTGGCTGTACCTAAGTATGTCAAAAAAC 1022
; ||| ||| ||| ||| ||| ||| ||| |||
; 179 .....AlaIleArgValThrGlnGlnAlaValTyrTyrTyrSerAspAsn 193
; ||| ||| ||| ||| ||| ||| ||| |||
; 1023 GCCCTGCCCTTTTCAGCATCAAGATGACGAGTGGGGGTCTATCTCAATGCC 1072

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2663 .....AACACCAAGGTGC..... 2677
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670  uProGluGlyTyrSerTyrLeuValLysGluThrAspSerGluGlyTyrL 687
      ||:::  |||  :::::  |||  :::::  |||
2678 .....GTTTCTTATACACATCAAGATATGATGTTAAGGGCAAT 2720
      :::::  |||  :::::  |||  :::::  |||
687  ysValLysValAsnSerGlnGluValAla..... 696
      :::::  |||  :::::  |||  :::::  |||
2721 TTTTGGCACAATGGCGAGAGTTGGCAGGACAGTTACATCATGACAAA 2770
      :::::  |||  :::::  |||  :::::  |||
697 .....AsnAlaThrValSerLysThrGly 704
      |||  |||  :::::  |||  :::::  |||
2771 GCGCATGGCATCAATGACACCGCCGAAAAAGCAGGG 2806

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